

GenCore version 5.1.3
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OM nucleic - nucleic search, using aw model

Run on: December 17, 2002, 15:35:20 ; Search time 3293 Seconds

(without alignments)
10755.577 Million cell updates/sec

Title: US-09-720-384A-3

Perfect score: 1217 (without alignments)

Sequence: 1 ggcgcgtttcttctca.....aaataaaaaaaaaaaaaa 1217

Scoring table:

CutOff Nuc Gapex 60.0, Gapex 60.0

Searched: 205640 seqs, 14551402878 residues

Word size: 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database:

GenBank:

1: gb.bai*

2: gb.hug*

3: gb.hug*

4: gb.con*

5: gb.ov*

6: gb.ov*

7: gb.ph*

8: gb.ph*

9: gb.ph*

10: gb.ro*

11: gb.tes*

12: gb.tes*

13: gb.vi*

14: gb.vi*

15: em.ba*

16: em.ba*

17: em.hum*

18: em.in*

19: em.in*

20: em.in*

21: em.or*

22: em.or*

23: em.ph*

24: em.ph*

25: em.ph*

26: em.ph*

27: em.tes*

28: em.un*

29: em.un*

30: em.tes*

31: em.tes*

32: em.tes*

33: em.tes*

34: em.tes*

35: em.tes*

36: em.tes*

37: em.tes*

38: em.tes*

39: em.tes*

40: em.tes*

41: em.tes*

Fred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	3.2	154330	2	AC104429
2	35	2.9	1053	3	AC104429
3	35	2.9	1053	3	AC104429
4	35	2.9	113680	3	PMALP4
5	35	2.9	116986	2	PMALP3
6	35	2.9	203610	2	AC102779
7	35	2.9	203610	2	AC102779
8	34	2.8	57	6	AX074093
9	34	2.8	57	6	AX074093
10	34	2.8	57	6	AX074093
11	34	2.8	50	3	AX192100
12	34	2.8	50	3	AX192100
13	34	2.8	50	3	AX192100
14	34	2.8	1627	9	BC036471
15	34	2.8	1627	9	BC036471
16	34	2.8	1627	9	BC036471
17	34	2.8	1508	6	AX045627
18	34	2.8	1508	6	AX045627
19	34	2.8	1508	6	AX045627
20	34	2.8	1508	6	AX045627
21	34	2.8	1508	6	AX045627
22	34	2.8	1508	6	AX045627
23	34	2.8	1508	6	AX045627
24	34	2.8	1508	6	AX045627
25	34	2.8	1508	6	AX045627
26	34	2.8	1508	6	AX045627
27	34	2.8	1508	6	AX045627
28	34	2.8	1508	6	AX045627
29	34	2.8	1508	6	AX045627
30	34	2.8	1508	6	AX045627
31	34	2.8	1508	6	AX045627
32	34	2.8	1508	6	AX045627
33	34	2.8	1508	6	AX045627
34	34	2.8	1508	6	AX045627
35	34	2.8	1508	6	AX045627
36	34	2.8	1508	6	AX045627
37	34	2.8	1508	6	AX045627
38	34	2.8	1508	6	AX045627
39	34	2.8	1508	6	AX045627
40	34	2.8	1508	6	AX045627
41	34	2.8	1508	6	AX045627
42	34	2.8	1508	6	AX045627
43	34	2.8	1508	6	AX045627
44	34	2.8	1508	6	AX045627
45	34	2.8	1508	6	AX045627

ALIGNMENTS

Result No.	Score	Query Match	Length	DB ID	Description
1	39	3.2	154330	2	AC104429
2	35	2.9	1053	3	AC104429
3	35	2.9	1053	3	AC104429
4	35	2.9	113680	3	PMALP4
5	35	2.9	116986	2	PMALP3
6	35	2.9	203610	2	AC102779
7	35	2.9	203610	2	AC102779
8	34	2.8	57	6	AX074093
9	34	2.8	57	6	AX074093
10	34	2.8	57	6	AX074093
11	34	2.8	50	3	AX192100
12	34	2.8	50	3	AX192100
13	34	2.8	50	3	AX192100
14	34	2.8	1627	9	BC036471
15	34	2.8	1627	9	BC036471
16	34	2.8	1627	9	BC036471
17	34	2.8	1508	6	AX045627
18	34	2.8	1508	6	AX045627
19	34	2.8	1508	6	AX045627
20	34	2.8	1508	6	AX045627
21	34	2.8	1508	6	AX045627
22	34	2.8	1508	6	AX045627
23	34	2.8	1508	6	AX045627
24	34	2.8	1508	6	AX045627
25	34	2.8	1508	6	AX045627
26	34	2.8	1508	6	AX045627
27	34	2.8	1508	6	AX045627
28	34	2.8	1508	6	AX045627
29	34	2.8	1508	6	AX045627
30	34	2.8	1508	6	AX045627
31	34	2.8	1508	6	AX045627
32	34	2.8	1508	6	AX045627
33	34	2.8	1508	6	AX045627
34	34	2.8	1508	6	AX045627
35	34	2.8	1508	6	AX045627
36	34	2.8	1508	6	AX045627
37	34	2.8	1508	6	AX045627
38	34	2.8	1508	6	AX045627
39	34	2.8	1508	6	AX045627
40	34	2.8	1508	6	AX045627
41	34	2.8	1508	6	AX045627
42	34	2.8	1508	6	AX045627
43	34	2.8	1508	6	AX045627
44	34	2.8	1508	6	AX045627
45	34	2.8	1508	6	AX045627

Fred. No. is the number of results predicted by chance to have a

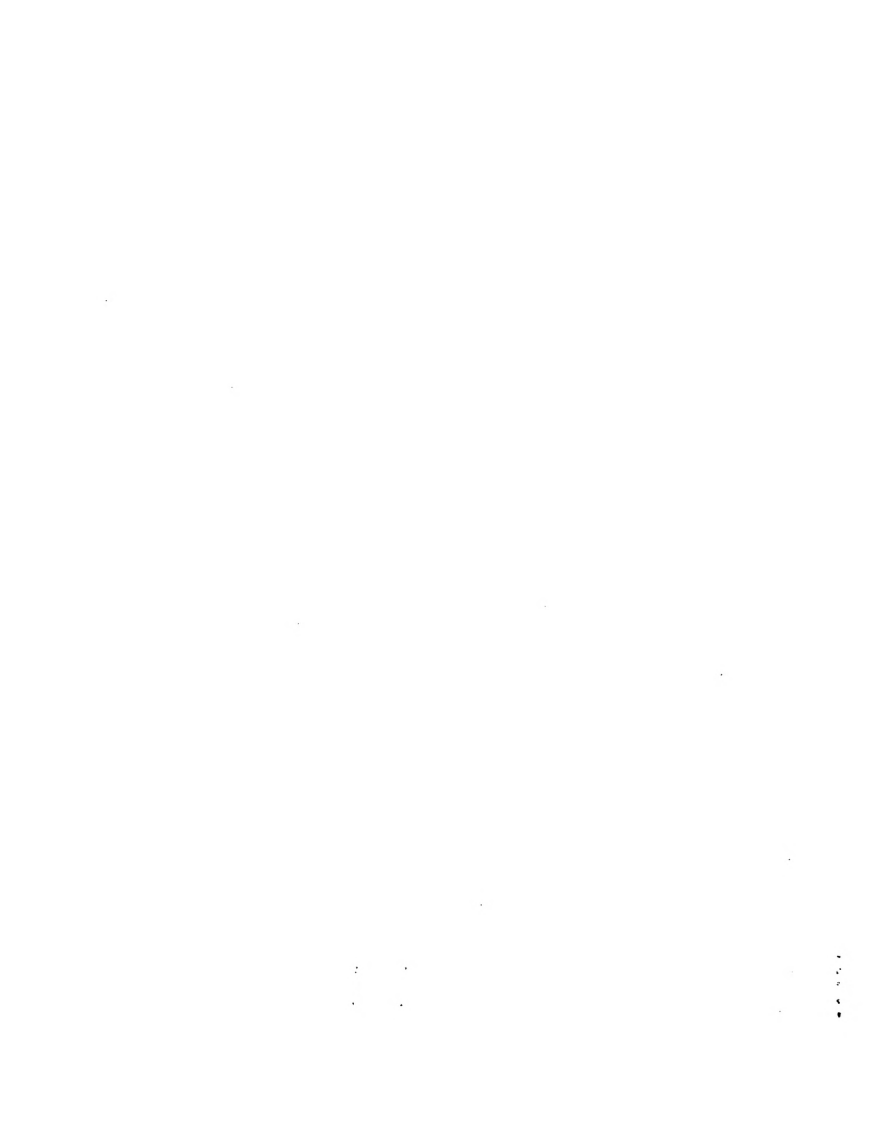
CC (congenital anomalies), endometriosis, breast (chronic mastitis), thyroid
 CC gland (Hashimoto's thyroiditis), adrenal gland, skin (psoriasis),
 CC osteoporosis. The compositions promote cell death and are useful for
 CC treating and/or ameliorating cancer and autoimmune diseases. The
 CC compositions as described herein are useful for treating and/or
 CC organ caused by infection which induce cell death. (1) is useful to
 CC raise an immune response, as a reagent in assays designed to
 CC quantitatively determine levels of the protein in biological fluids, as
 CC to isolate receptors or ligands. AAS6297-AAS6342 represent the
 CC protective polynucleotide sequences as described in the invention.

80 Sequence 116 BP; 73 A; 18 C; 11 G; 14 T; 0 other;

Query Match 2 78, Score 33, BB 24; Length 116;
 Best Local Similarity 100.0%, Pred. No. 0.0024;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1185 GTTTAATAAAAAAAAAAAAAAAAAAAAAAAAAA 1217
 DB 50 GTTTAATAAAAAAAAAAAAAAAAAAAAAAAAAA 82

Search completed: December 17, 2002, 17:47:35
 Job time : 310 secs



[illegible]

```

001 RESULT 3
002 US-9876-492A-2
003 Sequence 1; Application US/08379482A
004 Patent No.: A689314
005 APPLICANT: Burglerts, Filipe
006 APPLICANT: Holton, Timothy A. REFERENCES RECORDING
007 TITLE OF INVENTION: GLYCOSYLTRANSFERASE ENZYMS AND USES THEREOF
008 NUMBER OF SEQUENCES: 7
009 ADDRESS: Andrew Scott, Murphy & Plessner
010 STREET: 400 Garden City Plaza
011 CITY: Garden City
012 STATE: NY
013 COUNTRY: USA
014 ZIP: 11530
015 COMPUTER PROGRAM FORM:
016 MEDIUM TYPE: Floppy disk
017 COMPILED BY: JIM PC COMPILERS INC.
018 SOFTWARE: Precomp Release #1.0 Version #1.30
019 CURRENT APPLICATION DATA:/08/79_492A
020 FILING DATE: 38-JUL-1993
021 CLASSIFICATION: B00
022 NAME: DIGITAL; Frank S.
023 REGISTRATION NUMBER: 31,346
024 TELEPHONE:(316)743-4343
025 INFORMATION FOR SEQ ID NO: 2:
026 SOURCE CHARACTERISTICS:
027 type: nucleic acid
028 STRANDNESS: single
029 MOLECULE TYPE: DNA (genomic)
030 FEATURE: CDS
031 LOCATION: 1..1413
032 US-08-79-492A-2
033 Query Match 2.7% Score 33; DB 2; Length 1739;
034 Basic Local Similarity 100.0%; Emd No. 1.9e+05; Indexes 0; Caps 0
035 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0
036 Qy 1188 GTTATTATTTGGGCTGTTCAGTGCGGCACCAAAATTA 1217
037 1687 GTTATTTTATTTTTTTTATTTTATTTTGA 1699

```



```

1 COMPUTER READABLE FORM.
2 MEDIUM TYPE: Diskette
3 COMPUTER: IBM Compatible
4 SOFTWARE: FIELSEQ for Windows Version 2.0
5 CURRENT APPLICATION DATA: 09/09/438
6 FILING DATE: 20-JAN-1998
7 CLASSIFICATION: DATA
8 PRAISE/SLUG: DATA
9 APPLICATION NUMBER:
10 FILING DATE:
11 ATTORNEY/AGENT INFORMATION:
12 REGISTRATION NUMBER: 23,031
13 REFERENCE/DOCKET NUMBER: GH-70359
14 TELEPHONE: 610-407-0700
15 TELEFAX: 610-407-0701
16 INFORMATION FOR SEQ ID NO: 1:
17 SEQUENCE CHARACTERISTICS:
18 TYPE: nucleic acid
19 STRANDEDNESS: single
20 MOLECULE TYPE: RNA
21 US-09-009-438-1

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Query Match          2.7% Score 33; DB 2; Length 1910;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 1185 GTTTAAAAA.....AAAAAAAAA 1217
Db 1859 GTTTAAAAA.....AAAAAAAAA 1891

```

RESULT 5

```

1 SEQUENCE 5, Application US/09207493
2 Patent No. 643657
3 APPLICANT: Genentech, Inc.
4 APPLICANT: Sathe, Ganesha M.
5 APPLICANT: Halsey, Nandy S.
6 APPLICANT: OLP, Jeffrey S.
7 APPLICANT: Wang, Da-Yuan
8 TITLE OF INVENTION: ANTIBODIES OF SCREENING FOR MONITORS AND
9 RECEPTORS
10 FILE REFERENCE: GH70349-1 08/09/207,493
11 CURRENT FILING DATE: 1998-12-08
12 EARLIER APPLICATION NUMBER: 09/009,438
13 NUMBER OF SEQ ID NOS: 198-01-20
14 SOFTWARE: FIELSEQ for Windows Version 3.0
15 SEQ ID NO 1910
16 TYPE: DNA
17 ORGANISM: Human
18 US-09-207-493-1

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```

Query Match          2.7% Score 33; DB 3; Length 1910;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 1185 GTTTAAAAA.....AAAAAAAAA 1217
Db 1859 GTTTAAAAA.....AAAAAAAAA 1891

```

RESULT 6

```

1 US-09-445-558-35
2 Sequence 35, Application US/0946558
3 Patent No. 643657
4 APPLICANT: Genentech, Inc.
5 APPLICANT: Morikawa, Luyo O.
6 APPLICANT: Ozcoso Jr., Erali M.
7 FILE REFERENCE: 08/322 US NA
8 CURRENT APPLICATION NUMBER: US/09/445,558
9 PRAISE/SLUG: DATA
10 EARLIER APPLICATION NUMBER: 60/112,734
11 EARLIER FILING DATE: 1998-12-18
12 NUMBER OF SEQ ID NOS: 70
13 SEQ ID NO 35
14 ADDRESS: Biotechnology Office 97
15 LENGTH: 1961
16 ORGANISM: Oryza sativa
17 US-09-445-558-35

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Query Match          2.7% Score 33; DB 4; Length 1951;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1185 GTTTAAAAA.....AAAAAAAAA 1217
Db 1900 GTTTAAAAA.....AAAAAAAAA 1932

```

```

US-08-351-473B-1
Sequence 1, Application US/0835473B
Patent No. 643657
GENERAL INFORMATION:

```

```

1 APPLICANT: LENZEN, GERLINDA
2 APPLICANT: ADRIANO, ROBERTO
3 TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE
4 BOVINE BETA3-ADRENERGIC RECEPTOR AND THEIR APPLICATIONS
5 CROSS-REFERENCE TO RELATED APPLICATIONS
6 CROSS-REFERENCE TO PUBLISHED DOCUMENTS
7 ADDRESS/SEE: OBLON, SPIVAK, MCLELAND, WAIER & NEUSTADT
8 STREET: 34175 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
9 CITY: AUSTIN
10 STATE: VIRGINIA
11 COUNTRY: USA
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Floppy disk
14 SOFTWARE: FIELSEQ for Windows Version 3.0
15 OPERATING SYSTEM: PC-DOS/MS-DOS
16 SOFTWARE: Patent Release #1.0, Version #1.30
17 APPLICATION NUMBER: 08/351,473B
18 FILING DATE: 21-FEB-1995
19 PRAISE/SLUG: DATA
20 APPLICATION DATE:
21 APPLICATION NUMBER: 93 04670
22 FILING DATE: 21-APR-1993
23 REFERENCE TO OTHER PUBLICATIONS: PCT/EP94/00447
24 APPLICATION NUMBER:
25 FILING DATE: 21-APR-1994
26 FILING DATE: 21-APR-1994
27 NAME: OBLON, NORMAN F.
28 NAME: OBLON, NORMAN F.
29 REGISTRATION NUMBER: 24,618
30 TELEPHONE: 703-595-901-001 PCT
31 TELEPHONE: (703) 431-3000
32 TELEFAX: (703) 431-3220
33 TELEFAX: 24680 08 75
34 INFORMATION FOR SEQ ID NO: 1:
35 SEQUENCE CHARACTERISTICS:
36 TYPE: nucleic acid

```



```

Query Match
Best Local Similarity 100.0%, Pred. No. 1.8e-05; DB 4; Length 3410;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1185 GTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1217
Db 3322 GTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3354

RESULT 11
US-09-030-607-110
; Sequence 110, Application US/09030607
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun C.
; INVENTOR: Dillon, Devin C.; Harlocker, Susan L.;
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS: Array LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; CONTACT: 206-461-8600
; MEDIUM TYPE: Plasmid disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SERIAL NUMBER: 1,234,567
; CURRENT APPLICATION DATA: Sequence #1.0, Version #1.30
; APPLICATION NUMBER: US/09/030.607
; PRIORITY: 09-030-607
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C3
; TELEPHONE: (206) 682-6031
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 110:
; LENGTH: 3410 base pairs
; TYPE: nucleic acid
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORGANISM: Homo sapiens
US-09-030-607-110

Query Match
Best Local Similarity 100.0%, Pred. No. 1.8e-05; DB 4; Length 3410;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1185 GTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1217
Db 3322 GTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3354

RESULT 12
US-09-605-785-110
; Sequence 110, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun C.
; INVENTOR: Dillon, Devin C.; Harlocker, Susan L.;
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS: Array LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; CONTACT: 206-461-8600
; MEDIUM TYPE: Plasmid disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SERIAL NUMBER: 1,234,567
; CURRENT APPLICATION DATA: Sequence #1.0, Version #1.30
; APPLICATION NUMBER: US/09/030.607
; PRIORITY: 09-030-607
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C3
; TELEPHONE: (206) 682-6031
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 110:
; LENGTH: 3410 base pairs
; TYPE: nucleic acid
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORGANISM: Homo sapiens
US-09-605-785-110

Query Match
Best Local Similarity 100.0%, Pred. No. 1.8e-05; DB 4; Length 3410;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1185 GTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1217
Db 3322 GTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3354

RESULT 13
US-09-439-313-110
; Sequence 110, Application US/09439313
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun C.
; INVENTOR: Dillon, Devin C.; Harlocker, Susan L.;
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS: Array LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; CONTACT: 206-461-8600
; MEDIUM TYPE: Plasmid disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SERIAL NUMBER: 1,234,567
; CURRENT APPLICATION DATA: Sequence #1.0, Version #1.30
; APPLICATION NUMBER: US/09/030.607
; PRIORITY: 09-030-607
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C3
; TELEPHONE: (206) 682-6031
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 110:
; LENGTH: 3410 base pairs
; TYPE: nucleic acid
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORGANISM: Homo sapiens
US-09-439-313-110

Query Match
Best Local Similarity 100.0%, Pred. No. 1.8e-05; DB 4; Length 3410;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1185 GTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1217
Db 3322 GTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3354

RESULT 14
US-09-352-616A-110
; Sequence 110, Application US/09352616A

```

```

; APPLICANT: Fanger, Gary R.
; APPLICANT: Rafter, Marc W.
; APPLICANT: Bock, John A.
; APPLICANT: C.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Wang, Ailun
; APPLICANT:
; APPLICANT: Selsky, Yaelir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; NUMBER OF SEQUENCES: 224
; CURRENT APPLICATION NUMBER: US/09/605,785
; CURRENT FILING DATE: 2000-06-27
; INVENTOR: Xu, Jiangchun C.
; SOFTWARE: SEQ ID NOS: 835
; SEQ ID NO 110
; LENGTH: 3410
; ORGANISM: Homo sapiens
US-09-605-785-110

Query Match
Best Local Similarity 100.0%, Pred. No. 1.8e-05; DB 4; Length 3410;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1185 GTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1217
Db 3322 GTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3354

RESULT 13
US-09-439-313-110
; Sequence 110, Application US/09439313
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun C.
; INVENTOR: Dillon, Devin C.; Harlocker, Susan L.;
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS: Array LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; CONTACT: 206-461-8600
; MEDIUM TYPE: Plasmid disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SERIAL NUMBER: 1,234,567
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 2000-06-27
; INVENTOR: Xu, Jiangchun C.
; SOFTWARE: SEQ ID NOS: 835
; SEQ ID NO 110
; LENGTH: 3410
; ORGANISM: Homo sapiens
US-09-439-313-110

Query Match
Best Local Similarity 100.0%, Pred. No. 1.8e-05; DB 4; Length 3410;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1185 GTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1217
Db 3322 GTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3354

RESULT 14
US-09-352-616A-110
; Sequence 110, Application US/09352616A

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; FILE REFERENCE: 210121.487
; CURRENT APPLICATION NUMBER: US/09/867,701
; NUMBER OF FILING DATES: 2001-05-29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9612
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-867-701-9612

Query Match      2.7k; Score 33; DB 10; Length 178;
Local Similarity 100.0k; Pred. No. 0.0015
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1185 GTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1217
Db 90 GTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 122

RESULT 7
US-09-867-701-10381/c Application US/09867701
; Patent No. US020112217A1
; GENERAL INFORMATION: Paul A.
; APPLICANT: Adams, Robert
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.487
; CURRENT APPLICATION NUMBER: US/09/867,701
; NUMBER OF FILING DATES: 2001-05-29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10381
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-867-701-10381

Query Match      2.7k; Score 33; DB 10; Length 304;
Local Similarity 100.0k; Pred. No. 0.0015
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1185 GTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1217
Db 44 GTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 12

RESULT 8
US-09-791-242/c Application US/09770791
; Patent No. US20020062014A1
; GENERAL INFORMATION: Jom
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Ramesh, Scott L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Yu, Yang Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthews, Abraham V.
; APPLICANT: Hossain, Geoffrey P.
; APPLICANT: Hossain, Geoffrey P.
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Hoffmann, Neil

```

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; APPLICANT: Hurlan, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 210121.487
; CURRENT APPLICATION NUMBER: US/09/770,791
; NUMBER OF FILING DATES: 2001-01-26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 999
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-791-608

Query Match      2.7k; Score 33; DB 10; Length 356;
Local Similarity 100.0k; Pred. No. 0.0013
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1185 GTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1217
Db 35 GTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3

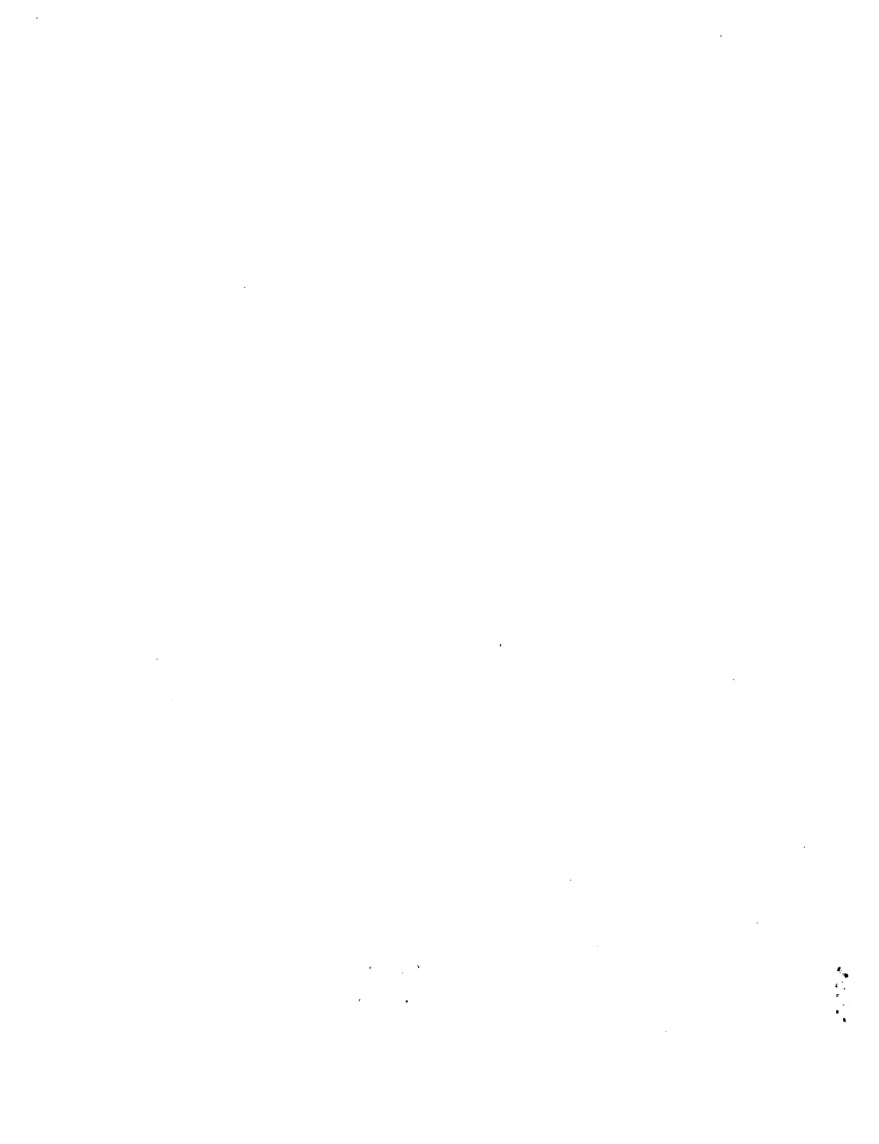
RESULT 9
US-09-360-352-5390/c Application US/0960352
; Patent No. US2002013719A1
; GENERAL INFORMATION: Warren, Wesley C.
; APPLICANT: Tao, Neungling
; APPLICANT: Matlialagan, Nageshpan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 1851.056/3-23102981
; CURRENT APPLICATION NUMBER: US/09/560,352
; NUMBER OF FILING DATES: 2001-09-24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5390
; TYPE: DNA
; ORGANISM: Bos taurus
US-09-360-352-5390

Query Match      2.7k; Score 33; DB 10; Length 362;
Local Similarity 100.0k; Pred. No. 0.0013
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1185 GTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1217
Db 106 GTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 74

RESULT 10
US-09-770-791-242/c Application US/09770791
; Patent No. US20020062014A1
; GENERAL INFORMATION: Jom
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Ramesh, Scott L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Yu, Yang Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthews, Abraham V.
; APPLICANT: Hossain, Geoffrey P.
; APPLICANT: Hossain, Geoffrey P.
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Hoffmann, Neil

```

BASE COUNT 199 a 121 c 154 g 225 t
 ORIGIN Clones to be sequenced were prepared by mass excision. *

Query Match 5.6%; Score 68; DB 10; Length 699;
 Best Local Similarity 100.0%; Pred. No. 5e-07;
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 717 TCAATCATCTAGCTTACTTATCTATCTATCAAGAGAAATGATGATCGCTGCTC 716
 DB 32 TCAATCATCTAGCTTACTTATCTATCTATCTATCAAGAGAAATGATGATCGCTGCTC 91
 DB 92 TACTTCCA 99

RESULT 9
 AM22946
 DEFINITION DOL 47 B4 A02 Dark Green 1 (DGL) Sorghum bicolor CNNA, RNA
 ACCESSION AM22946
 VERSION 1
 KEYWORDS EST
 SOURCE sorghum bicolor
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 1 (bases 1 to 721); Andropogoneae; Sorghum.

REFERENCE Cordumier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt
 AUTHORS
 JOURNAL Unpublished (2000)
 COMMENT Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Fax: 706 583 0210
 Email: mpratt@uga.edu
 Clones to be sequenced were prepared by mass excision.
 below Phred quality 16. The threshold for highest quality sequence
 is 20.

FEATURES
 source 1..721
 /organism="Sorghum bicolor"
 /clone_lib="dark green 1 (DGL)"
 /notes="Organ: 5-day-old dark-grown seedlings. Vector:
 made from poly-A RNA in the cloning vector lambda Zap II.
 Clones to be sequenced were prepared by mass excision."
 BASE COUNT 202 a 114 c 181 g 234 t

Query Match 5.6%; Score 68; DB 10; Length 721;
 Best Local Similarity 100.0%; Pred. No. 4.9e-07;
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 717 TCAATCATCTAGCTTACTTATCTATCTATCAAGAGAAATGATGATCGCTGCTC 716
 DB 41 TCAATCATCTAGCTTACTTATCTATCTATCTATCAAGAGAAATGATGATCGCTGCTC 100
 DB 92 TACTTCCA 99

RESULT 9
 AM22946
 DEFINITION DOL 47 B4 A02 Dark Green 1 (DGL) Sorghum bicolor CNNA, RNA
 ACCESSION AM22946
 VERSION 1
 KEYWORDS EST
 SOURCE sorghum bicolor
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 1 (bases 1 to 721); Andropogoneae; Sorghum.

REFERENCE Cordumier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt
 AUTHORS
 JOURNAL Unpublished (2000)
 COMMENT Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Fax: 706 583 0210
 Email: mpratt@uga.edu
 Clones to be sequenced were prepared by mass excision.
 below Phred quality 16. The threshold for highest quality sequence
 is 20.

BASE COUNT 199 a 121 c 154 g 225 t
 ORIGIN Clones to be sequenced were prepared by mass excision. *

Query Match 5.6%; Score 68; DB 10; Length 699;
 Best Local Similarity 100.0%; Pred. No. 5e-07;
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 717 TCAATCATCTAGCTTACTTATCTATCTATCAAGAGAAATGATGATCGCTGCTC 716
 DB 32 TCAATCATCTAGCTTACTTATCTATCTATCTATCAAGAGAAATGATGATCGCTGCTC 91
 DB 92 TACTTCCA 99

RESULT 9
 AM22946
 DEFINITION DOL 47 B4 A02 Dark Green 1 (DGL) Sorghum bicolor CNNA, RNA
 ACCESSION AM22946
 VERSION 1
 KEYWORDS EST
 SOURCE sorghum bicolor
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 1 (bases 1 to 746); Andropogoneae; Sorghum.

REFERENCE Cordumier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt
 AUTHORS
 JOURNAL Unpublished (2000)
 COMMENT Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Fax: 706 583 0210
 Email: mpratt@uga.edu
 Clones to be sequenced were prepared by mass excision.
 below Phred quality 16. The threshold for highest quality sequence
 is 20.

FEATURES
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 /organism="Sorghum bicolor"
 /clone_lib="dark green 1 (DGL)"
 /notes="Organ: 5-day-old dark-grown seedlings. Vector:
 made from poly-A RNA in the cloning vector lambda Zap II.
 Clones to be sequenced were prepared by mass excision."
 BASE COUNT 218 a 118 c 168 g 236 t

Query Match 5.6%; Score 68; DB 10; Length 746;
 Best Local Similarity 100.0%; Pred. No. 4.9e-07;
 Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 717 TCAATCATCTAGCTTACTTATCTATCTATCAAGAGAAATGATGATCGCTGCTC 716
 DB 54 TCAATCATCTAGCTTACTTATCTATCTATCTATCAAGAGAAATGATGATCGCTGCTC 113
 DB 114 TACTTCCA 121

RESULT 11
 A1987561
 LOCUS A1987561.1
 DEFINITION A1987561.1
 ACCESSION A1987561.1
 VERSION 1
 KEYWORDS EST
 SOURCE Zea mays
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade: Penicillaceae; Andropogoneae; Zea
 1 (bases 1 to 503)

REFERENCE Malbot,V.
 AUTHORS


```

ORIGIN
Query Match      3.1%; Score 38; DB 17; Length 741;
Local Similarity 10.0%; Predicted 12.1;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 647 AACGCGAAGCGCGGCAAAATATCCAGAGCTGCT 695
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Db 349 AAAGCGAAGACCTGCGAAAATATACAGAGCTTGT 311
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RESULT 14
AM22862
DEFINITION D01.47 B04_b1_A002 Dark Grown 1 (DGI) Sorghum bicolor cDNA, mRNA
sequence.
ACCESSION AM22862.1
VERSION AM22862.1 GI:8098687
KEYWORDS EST.
SOURCE Sorghum bicolor
ORGANISM Sorghum bicolor

Bakayota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
Cordonnier-Pratt M.-M., Gingle A., Marsala, C., Sudman M. and Pratt
L.H.
Unpub database from Sorghum dark-grown seedlings
Unpublished (2000)
Contact: Cordonnier-Pratt MW
Department of Genetics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel.: 706 542 3860
Fax: 706 542 0210
Email: mpratt@uga.edu
Sequences have been trimmed to exclude polyA, vector and regions
Below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: JEN REV
High quality sequence stop: 161
POVA-No. 1. 162
Location/Qualifiers
1. /organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone_lib="Dark Grown 1 (DGI)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap; Site 1: XhoI; Site 2: EcoRI; This library was
made from polyA RNA in the cloning vector lambda Zap 11.
Clones to be sequenced were prepared by mass excision."
Cloned 21 a 71 c 55 b 22 t prepared by mass excision. 11.
BASE COUNT 21 a 71 c 55 b 22 t
ORIGIN
Query Match      3.1%; Score 38; DB 10; Length 169;
Local Similarity 100.0%; Predicted 14;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 206 CCGCCCTGTCATCCATCCCTCCCTCCCTCCCTTC 243
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Db 75 CCGCCCTGTCATCCATCCCTCCCTCCCTCCCTTC 116
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Search completed: December 17, 2002, 19:23:00
Job time : 2414 secs

ORIGIN
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Local Similarity 10.0%; Predicted 12.1;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 206 CCGCCCTGTCATCCATCCCTCCCTCCCTCCCTTC 243
|||||
Db 67 CCGCCCTGTCATCCATCCCTCCCTCCCTCCCTTC 104
|||||

RESULT 15
BE35228
DEFINITION D01_113 B07_b1_A002 Dark Grown 1 (DGI) Sorghum bicolor cDNA, mRNA
sequence.
ACCESSION BE35228.1
VERSION BE35228.1 GI:9296332
KEYWORDS EST.
SOURCE Sorghum bicolor
ORGANISM Sorghum bicolor

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Bakayota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
Cordonnier-Pratt M.-M., Gingle A., Marsala, C., Sudman M. and Pratt
L.H.
Unpub database from Sorghum dark-grown seedlings
Unpublished (2000)
Contact: Cordonnier-Pratt MW
Department of Genetics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel.: 706 542 3860
Fax: 706 542 0210
Email: mpratt@uga.edu
Sequences have been trimmed to exclude polyA, vector and regions
Below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: JEN REV
High quality sequence stop: 168
POVA-No. 1. 162
Location/Qualifiers
1. /organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone_lib="Dark Grown 1 (DGI)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap; Site 1: XhoI; Site 2: EcoRI; This library was
made from polyA RNA in the cloning vector lambda Zap 11.
Clones to be sequenced were prepared by mass excision. 11.
BASE COUNT 21 a 71 c 55 b 22 t prepared by mass excision. 11.
ORIGIN
Query Match      3.1%; Score 38; DB 10; Length 169;
Local Similarity 100.0%; Predicted 14;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 206 CCGCCCTGTCATCCATCCCTCCCTCCCTCCCTTC 243
|||||
Db 75 CCGCCCTGTCATCCATCCCTCCCTCCCTCCCTTC 116
|||||

Search completed: December 17, 2002, 19:23:00
Job time : 2414 secs

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